

FEATURES Source Location/Qualifiers
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 74.0%; Score 14.8; DB 6; Length 47;
 Best Local Similarity 80.0%; Pred. No. 1.1e+04; Mismatches 3; Indels 0; Gaps 0;
 Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 AACATGTAACCTTGGTCA 20
 Db 33 AACATGTAACCTTGGTCA 14

RESULT 2

AR411025 AR411025 43 bp DNA linear PAT 18-DEC-2003

LOCUS Sequence 14 from patent US 6635475. DNA linear PAT 05-DEC-1998

DEFINITION Sequence 14 from patent US 6635475.

ACCESSION AR411025

VERSION AR411025.1 GI:40162603

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 43)

TITLE Helmann,J.D.

JOURNAL Patent: US 6635475-A 14 21-OCT-2003;

FEATURES Source Location/Qualifiers

1. 43
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 69.0%; Score 13.8; DB 6; Length 43;
 Best Local Similarity 88.2%; Pred. No. 3.5e+04; Mismatches 2; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACATGTAACCTTGG 17
 Db 1 AACATGTAACCTTGG 17

RESULT 3

AR805034/c AR805034 25 bp DNA linear PAT 25-NOV-2003

LOCUS Sequence 1202 from Patent WO03060160. DNA linear PAT 05-DEC-1998

DEFINITION Sequence 1202 from Patent WO03060160.

ACCESSION AR805034

VERSION AR805034.1 GI:36522175

KEYWORDS

SOURCE Oreochromis niloticus (Nile tilapia)

ORGANISM Oreochromis niloticus
 Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Buteloosteii; Neoteleosteii;
 Acanthomorpha; Acanthopterygii; Perciformes;
 Labroidei; Cichlidae; Oreochromis.

REFERENCE

AUTHORS 1 Paul,J. and Trueheart,J.

TITLE Yeast cells engineered to produce pheromone system protein
 surrogates, and uses therefore

JOURNAL Patent: WO 03060160-A 24-07-2003;

FEATURES Source Location/Qualifiers

1. 25
 /organism="Oreochromis niloticus"
 /mol_type="unassigned DNA"
 /db_xref="taxon:8128"

ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 35;
 Best Local Similarity 80.0%; Pred. No. 4.4e+04; Mismatches 4; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AACATGTAACCTTGGTCA 20
 Db 20 AACATGTAACCTTGGTCA 1

RESULT 6

AR160260/c AR160260 35 bp DNA linear PAT 17-OCT-2001

LOCUS Sequence 6 from patent US 6255059. DNA linear PAT 17-OCT-2001

DEFINITION Sequence 6 from patent US 6255059.

ACCESSION AR160260

VERSION AR160260.1 GI:16223904

KEYWORDS

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 33)

TITLE Tripp,C.Ann. and Wieneowski,N.

JOURNAL Patent: US 578194-A 11-04-Aug-1998;

FEATURES Source Location/Qualifiers

1. 33
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 69.0%; Score 13.6; DB 6; Length 33;
 Best Local Similarity 80.0%; Pred. No. 4.4e+04; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AACATGTAACCTTGG 20
 Db 13 AACATGTAACCTTGG 32

RESULT 5

AR020629/c AR020629 35 bp DNA linear PAT 05-DEC-1998

LOCUS Sequence 15 from patent US 578194. DNA linear PAT 05-DEC-1998

DEFINITION Sequence 15 from patent US 578194.

ACCESSION AR020629

VERSION AR020629.1 GI:397244

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE

AUTHORS 1 (bases 1 to 35)

TITLE Paul,J. and Trueheart,J.

JOURNAL Patent: US 578184-A 15-04-Aug-1998;

FEATURES Source Location/Qualifiers

1. 35
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 35;
 Best Local Similarity 80.0%; Pred. No. 4.4e+04; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AACATGTAACCTTGGTCA 20
 Db 20 AACATGTAACCTTGGTCA 1

SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED Unclassified.
 REFERENCE 1 (bases 1 to 35)
 AUTHORS Klein,C.A., Murphy,A.J.M., Powles,D.M., Broach,J., Manfredi,J.,
 TITLE Methods for identifying G protein coupled receptor effectors
 JOURNAL Patent: US 6250595-A 6-03-JUL-2001;
 FEATURES source
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 1..35
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

RESULT 7

Query Match 68.0%; Score 13.6; DB 6; Length 35;
 Best Local Similarity 80.0%; Pred. No. 4.4e+04; Mismatches 4; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AACATGTAACTTTGGCA 20

Db 20 AACATGTAACTTTGGCA 1

ORIGIN

RESULT 9

Query Match 67.0%; Score 13.4; DB 6; Length 24;
 Best Local Similarity 93.3%; Pred. No. 5.6e+04; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ATGAACTTGGC 19

Db 8 ATGAACTTGGC 22

ORIGIN

RESULT 10

Query Match 67.0%; Score 13.4; DB 6; Length 40;
 Best Local Similarity 87.5%; Pred. No. 5.6e+04; Mismatches 2; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACATGTAACTTTGG 17

Db 14 AACATGTAACTTG 29

ORIGIN

RESULT 11

Query Match 68.0%; Score 13.6; DB 6; Length 43;
 Best Local Similarity 80.0%; Pred. No. 4.4e+04; Mismatches 4; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AACATGTAACTTTGGCA 20

Db 11 AACATGTAACTTTGGCA 30

ORIGIN

RESULT 8

Query Match 67.0%; Score 13.4; DB 6; Length 40;
 Best Local Similarity 87.5%; Pred. No. 5.6e+04; Mismatches 2; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACATGTAACTTTGG 17

Db 14 AACATGTAACTTG 29

ORIGIN

Query Match 67.0%; Score 13.4; DB 6; Length 40;
 Best Local Similarity 87.5%; Pred. No. 5.6e+04; Mismatches 2; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACATGTAACTTG 17

Db 14 AACATGTAACTTG 29

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RESULT 11	source		/organism="synthetic construct"
BD089416/c	BD089416	22 bp	DNA
LOCUS	A method of arraying genome clone.		linear
DEFINITION			PAT 27-AUG-2002
ACCESSION	BD089416		
VERSION	BD089416_1		
KEYWORDS	JP 2001321190-A/1650		
SOURCE	Synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	1 (bases 1 to 22)		
AUTHORS	Soeda, E.		
TITLE	A method of arraying genome clone		
JOURNAL	Patent: JP 2001321190-A_1650 20-Nov-2001;		
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA			
GENOTECHS			
COMMENT			
OS	Artificial Sequence		
PN	JP 2001321190-A/1660		
PD	20-NOV-2001		
PI	EIICHI SOEDA		
PC	C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N33/53, G01N33/566, PC		
CC	C12N15/00		
QC	Description of Artificial Sequence: Synthetic DNA FH	Key	
FT	source	1. -22	
FEATURES	/organism="Artificial Sequence",		
source	1. -22		
FT	Location/Qualifiers		
PI	Location/Qualifiers		
CC	1. -22		
ORIGIN			
RESULT 12			
BD089578/c			
LOCUS	BD089578	66.0%	Score 13.2;
DEFINITION	A method of arraying genome clone.	DB 6;	Length 22;
ACCESSION	BD089578	Pred. No. 7.1e+04;	
VERSION	BD089578_1	Mismatches 0;	
KEYWORDS	JP 2001321190-A/1822,	Indels 0;	
SOURCE	synthetic construct	Gaps 0;	
ORGANISM	synthetic construct		
REFERENCE	1 (bases 1 to 22)		
AUTHORS	Soeda, E.		
JOURNAL	Patent: JP 2001321190-A_1822 20-Nov-2001;		
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA			
GENOTECHS			
COMMENT			
OS	Artificial Sequence		
PN	JP 2001321190-A/1822		
PD	20-NOV-2001		
PI	EIICHI SOEDA		
PC	C12N15/00, C12N15/09, C12M1/00, C12Q1/68, G01N33/53, G01N33/566, PC		
CC	Description of Artificial Sequence: Synthetic DNA FH	Key	
FT	source	1. -22	
RESULT 13			
AB068139/c			
LOCUS	AB068139	66.0%	Score 13.2;
DEFINITION	Synthetic construct DNA, reverse primer for human STS	DB 6;	Length 22;
ACCESSION	AB068139	STS-stdGDB43043 at 1P36.	
VERSION	AB068139_1	GI:15158943	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE	1		
AUTHORS	Chen, Y. Z., Hayashi, Y., Wu, J. G., Takaoka, E., Maekawa, K., Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H., Morohashi, A., Onira, M., Nakawara, A., Liu, S., Hoshi, M., Hori, A., and Soeda, E.		
TITLE	A BAC-based STS-concentric map spanning a 35-Mb region of human chromosome 1P35-P36		
JOURNAL	Genomics 74 (1), 55-70 (2001)		
MEDLINE	21269192		
PUBMED	11374902		
REFERENCE	2 (bases 1 to 22)		
AUTHORS	Hori, A.		
TITLE	Direct Submission		
JOURNAL	Submitted 104-AUG-2001; Akira Hori, Tohoku University School of Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-Ku, Sendai, Miyagi 980-8575, Japan (E-mail: hori@ml.cc.tohoku.ac.jp, Tel: 81-22-717-8042, Fax: 81-22-717-8047)		
FEATURES			
source	1. -22		
RESULT 14			
AB068145/c			
LOCUS	AB068145	66.0%	Score 13.2;
DEFINITION	Synthetic construct DNA, reverse primer for human STS sts-stdGDB43043 at 1P36	DB 12;	Length 22;
ACCESSION	AB068145		

VERSION AB068145.1 GI:15128949
 KEYWORDS synthetic construct
 SOURCE
 ORGANISM synthetic construct
 REFERENCE
 AUTHORS
 TITLE A BAC-based STS-content map spanning a 35-Mb region of human
 JOURNAL Chromosome 1P35-p36
 MEDLINE Genomics 74 (1), 55-70 (2001)
 PUBMED 11374902
 REFERENCE
 AUTHORS Horii,A.
 TITLE Direct Submission
 JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
 Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
 Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp),
 Tel:81-22-717-8042, Fax:81-22-717-8047;
 FEATURES source
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="reverse Primer for human STS STS-A002035 at 1P36
 STS-A002035 Obtained from clones B262K21, B239K20, B215H8,
 B239P22, B239P22, B301O16, B262K21, Human BAC Library
 RPCI-11"
 ORIGIN
 Query Match 66.0%; Score 13.2; DB 12; Length 22;
 Best Local Similarity 83.3%; Pred. No. 7.1e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 ACATGACTTGTGCA 20
 Db 19 ACATGTAACATGTGGCA 2
 RESULT 15
 AJ589959/c AJ589959
 LOCUS AJ589959
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
 561B05.
 ACCESSION AJ589959
 VERSION AJ589959.1 GI:37339583
 KEYWORDS left border; T-DNA flanking sequence.
 SOURCE
 ORGANISM Arabidopsis thaliana (thale cress)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicots; core eudicot;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1
 AUTHORS Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
 Chauvin, S., Bechtold, N., Croud, C., DeRose, R., Pelletier, G.,
 Lepliec, L., Caboche, M., and Lecharny, A.
 TITLE T-DNA integration into the Arabidopsis genome depends on sequences
 of pre-insertion sites
 JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
 MEDLINE 22263535
 PUBMED 12446565
 REFERENCE 2 (bases 1 to 37)
 AUTHORS Balzergue,S.
 TITLE Direct Submission
 JOURNAL Submitted (23-OCT-2003) Balzergue, S., UMRGV, INRA/CNRS, 2 rue
 Gaston Cremieux, 91057 Evry Cedex, FRANCE
 COMMENT PCR was performed on DNA from transformants of *Arabidopsis thaliana*
 plants from INRA (versailles). The DNA fragment(s) resulting from
 the PCR were directly sequenced from the left or the right border

to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclins/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante.info.infobiogen.fr>).

FEATURES source
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /cultivar="Wassilewskija"
 /db_xref="taxon:3702"
 /clone="51B5"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /note="T-DNA flanking sequence
 1. .37
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 left border"
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 Best Local Similarity 83.3%; Pred. No. 7e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 AACATGACTTGTGCA 18
 Db 19 AACATGTAACATGTGGCA 2
 Search completed: March 27, 2004, 10:00:26
 Job time : 1558 secs

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OM nucleic - nucleic search, using sw model

Run on: March 27, 2004, 09:23:56 ; Search time 75 Seconds
(without alignments)
147.987 Million cell updates/sec

Title: US-10-006-191-48
Perfect score: 20
Sequence: 1. aaacatggtaacttttggtca 20

Scoring table: IDENTITY_NUC
Gappp 10.0 , Gapext 1.0

Searched: 682709 seqs, 2774/5446 residues

Total number of hits satisfying chosen parameters: 839752

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

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2: /cgn2_6/podata/2/ina/5B COMB. seq: *
3: /cgn2_6/podata/2/ina/6A COMB. seq: *
4: /cgn2_6/podata/2/ina/6B COMB. seq: *
5: /cgn2_6/podata/2/ina/PCITUS COMB. seq: *
6: /cgn2_6/podata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
C 1	14.8	74.0	47 4	US-09-422-978-2469
C 2	13.8	69.0	43 7	US-09-422-978-2469
C 3	13.6	68.0	33 1	US-08-450-944-11
C 4	13.6	68.0	33 5	PCT-US96-07709-11
C 5	13.6	68.0	35 1	US-08-464-511-15
C 6	13.6	68.0	35 2	US-08-461-988-15
C 7	13.6	68.0	35 3	US-08-322-131-15
C 8	13.6	68.0	35 3	US-08-502-333A-6
C 9	13.4	67.0	40 4	US-09-830-317-41
C 10	13.2	66.0	30 4	US-09-624-570-14
C 11	12.9	66.0	31 1	US-09-634-570-16
C 12	12.8	64.0	24 1	US-08-411-383-9
C 13	12.6	63.0	27 1	US-08-381-280-20
C 14	12.6	63.0	27 2	US-08-442-533-20
C 15	12.6	63.0	27 3	US-09-032-083-20
C 16	12.6	63.0	47 4	US-09-422-784-412
C 17	12.4	62.0	38 3	US-09-178-089-9
C 18	12.4	62.0	41 3	US-09-178-089-3
C 19	12.4	62.0	44 3	US-09-178-089-11
C 20	12.4	62.0	47 4	US-09-422-978-1022
C 21	12.2	61.0	30 3	US-09-142-078-51
C 22	12.2	61.0	30 4	US-09-317-41-51
C 23	12.2	61.0	30 4	US-09-533-89-51
C 24	12.2	61.0	30 4	US-09-142-080-51
C 25	12.2	61.0	31 3	US-09-142-078-59
C 26	12.2	61.0	31 3	US-09-317-41-59
C 27	12.2	61.0	31 3	US-09-533-889-59

RESULTS

RESULT 1
US-09-422-978-2469/c

Sequence 2469, Application US/09422978
Patent No. 6537751

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel
APPLICANT: Blumenthal, Marta
APPLICANT: Chumakov, Ilya

TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REFERENCE: GENOME.00CPI
CURRENT APPLICATION NUMBER: US/09-422-978

CURRENT FILING DATE: 1999-10-20

EARLIER APPLICATION NUMBER: US 09/1298, 850

EARLIER FILING DATE: 1999-04-21

EARLIER APPLICATION NUMBER: US 60/109, 732

EARLIER FILING DATE: 1998-11-23

EARLIER APPLICATION NUMBER: US 60/082, 614

EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 2469

LENGTH: 47

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE: Sequence

NAME/KEY: allele

LOCATION: 24

OTHER INFORMATION: 99-11179-239 : polymorphic base C or T

US-09-422-978-2469

Query Match 74.0%; Score 14.8; DB 4; Length 47;

Best Local Similarity 80.0%; Pred. No. 1.4e+02;

Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1. AAACATGGTACTTTGGTCA 20

Db 33 AAACATGGTACTTTGGTCA 14

SEQUENCE ALIGNMENTS

Sequence 59, Appli
Sequence 9, Appli
Sequence 87, Appli
Sequence 162, Appli
Sequence 162, Appli
Sequence 34, Appli
Sequence 821, Appli
Sequence 2964, Appli
Sequence 96, Appli
Sequence 152, Appli
Sequence 827, Appli
Sequence 162, Appli
Sequence 11, Appli
Sequence 45, Appli
Sequence 45, Appli
Sequence 7881, Appli
Sequence 13, Appli
Sequence 12, Appli

APPLICANT: Wisniewski, Nancy
 TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
 SEQ ID NO: 14
 LENGTH: 43
 TYPE: DNA
 ORGANISM: *Bacillus subtilis*
 US-09-627-746-14

Query Match 69.0%; Score 13.8; DB 4; Length 43;
 Best Local Similarity 88.2%; Pred. No. 4 4e+02; Indels 0; Gaps 0;
 Matches 15; Conservative 17; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACACATGAACTTTGG 17
 DB 1 AACATGAACTTTGG 17

RESULT 3
 US-08-450-944-11
 Sequence 11, Application US/08450944
 Patent No. 5789194
 GENERAL INFORMATION:
 APPLICANT: TRIPP, Cynthia A.
 APPLICANT: Wisniewski, Nancy
 TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sheridan Ross & McIntosh
 STREET: 1700 Lincoln St., Suite 3500
 CITY: Denver
 STATE: Colorado
 COUNTRY: U.S.A.
 ZIP: 80203

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: PCT/US96/07709
 FILING DATE: 23-MAY-1996
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Connell, Gary J.
 REGISTRATION NUMBER: 32, 020
 REFERENCE/DOCKET NUMBER: 2618-30-PCT

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 863-9700
 TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
 LENGTH: 33 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)

FEATURE:
 NAME/KEY: misc feature
 LOCATION: 1..33
 OTHER INFORMATION: /label= PRIMER

PCT-US96-07709-11

Query Match 68.0%; Score 13.6; DB 5; Length 33;
 Best Local Similarity 80.0%; Pred. No. 5.3e+02; Indels 0; Gaps 0;
 Matches 16; Conservative 20; Mismatches 4; Indels 0; Gaps 0;

QY 1 AACACATGAACTTTGGCA 20
 DB 13 AACATGAACTTTGGTA 32

RESULT 5
 US-08-464-511-15/c
 Sequence 15, Application US/08464531
 Patent No. 579184
 GENERAL INFORMATION:
 APPLICANT: FOMIKES, Dana M.
 APPLICANT: BROCH, Jim
 APPLICANT: MANIFIDI, John
 APPLICANT: KLEIN, Christine
 APPLICANT: MURPHY, Andrew J.
 APPLICANT: PAUL, Jeremy
 APPLICANT: TRUEHART, Joshua
 TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
 TITLE OF INVENTION: PHARMACEUTICAL PROTEIN SURROGATES, AND USES THEREFOR
 NUMBER OF SEQUENCES: 119
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

RESULT 4
 PCT-US96-07709-11
 Sequence 11, Application US/08464531
 GENERAL INFORMATION:
 APPLICANT: TRIPP, Cynthia A.

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/464,531
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/322,137
 FILING DATE: 13-OCT-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/309,313
 FILING DATE: 20-SEP-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/190,328
 FILING DATE: 31-JAN-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/041,431
 FILING DATE: 31-MAR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: COOPER, Iver P.
 REGISTRATION NUMBER: 28,005
 REFERENCE/DOCKET NUMBER: FOLWKES=2G
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 24633
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 35 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: synthetic DNA
 US-08-461-531-15
 Query Match 68 0%; Score 13.6; DB 1; Length 35;
 Best Local Similarity 80 0%; Pred. No. 5.3e+02; 4; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 4;
 Qy 1 AAACTGAACTTGTGCA 20
 Db 20 AACTAGTAATTTGATCA 1
 RESULT 6
 US-08-461-598-15/c
 Sequence 15, Application US/08461598
 Patent No. 5876951
 GENERAL INFORMATION:
 APPLICANT: FOMIKES, Dana M.
 APPLICANT: BROACH, Jim
 APPLICANT: MANFREDI, John
 APPLICANT: KLEIN, Christine
 APPLICANT: MURPHY, Andrew J.
 APPLICANT: PAUL, Jeremy
 APPLICANT: TRUEHEART, Joshua
 TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
 NUMBER OF SEQUENCES: 119
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/322,137
 FILING DATE: 13-OCT-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/309,313
 FILING DATE: 31-OCT-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/322,137
 FILING DATE: 20-SEP-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/190,328
 FILING DATE: 31-JAN-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/041,431
 FILING DATE: 31-MAR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: COOPER, Iver P.
 REGISTRATION NUMBER: 28,005
 REFERENCE/DOCKET NUMBER: FOLWKES=2G
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 24633
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 35 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: synthetic DNA
 US-08-461-598-15
 Query Match 68 0%; Score 13.6; DB 2; Length 35;
 Best Local Similarity 80.0%; Pred. No. 5.3e+02; 4; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 4;
 Qy 1 AAACTGAACTTGTGCA 20
 Db 20 AACTAGTAATTTGATCA 1
 RESULT 7
 US-08-322-137-15/c
 Sequence 15, Application US/08322137
 Patent No. 6100042
 GENERAL INFORMATION:
 APPLICANT: FOMIKES, Dana M.
 APPLICANT: BROACH, Jim
 APPLICANT: MANFREDI, John
 APPLICANT: KLEIN, Christine
 APPLICANT: MURPHY, Andrew J.
 APPLICANT: PAUL, Jeremy
 APPLICANT: TRUEHEART, Joshua
 TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
 NUMBER OF SEQUENCES: 119
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/322,137
 FILING DATE: 13-OCT-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/309,313
 FILING DATE: 20-SEP-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/190,328
 FILING DATE: 31-JAN-1994
 APPLICATION NUMBER: US 08/041,431
 FILING DATE: 31-MAR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: COOPER, Ivor P.
 REGISTRATION NUMBER: 28,005
 REFERENCE/DOCKET NUMBER: FOLMKES-2C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248633

INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 35 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: synthetic DNA
 US-08-333A-6/C

Query Match 68.0%; Score 13.6; DB 3; Length 35;
 Best Local Similarity 80.0%; Pred. No. 5.3e+02;
 Matches 16; Conservative 0; Mismatches 4;
 Qy 1 AACATGTAACTTTGCGCA 20
 Db 20 AACTAGTAATTGATCA 1

RESULT 8
 Sequence 6, Application US/08582333A
 Patent No. 6255059
 GENERAL INFORMATION:
 APPLICANT: Klein, Christine A.
 APPLICANT: Murphy, Andrew J. M.
 TITLE OF INVENTION: Methods and Compositions for
 NUMBER OF SEQUENCES: 98
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LARIVE & COCKFIELD
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/582,333A
 FILING DATE: 17-JAN-1996
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Catherine J. Kara
 REGISTRATION NUMBER: 41,106
 REFERENCE/DOCKET NUMBER: CPI-012CPS
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEX: (617) 227-4214

INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 35 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

RESULT 9
 Sequence 9, Application US/09930337
 Patent No. 6314706
 GENERAL INFORMATION:
 APPLICANT: von Kalle, Christof
 APPLICANT: Schmidt, Manfred
 TITLE OF INVENTION: LINEAR AMPLIFICATION MEDIATED PCR (=LAM PCR)
 FILE REFERENCE: 0147-0227P
 CURRENT APPLICATION NUMBER: US/09/830,337
 CURRENT FILING DATE: 2001-04-26
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 41
 LENGTH: 40
 TYPE: DNA
 ORGANISM: Macaca mulatta
 FEATURE:
 NAME/KEY: LTR
 LOCATION: (31)..(40)
 OTHER INFORMATION: The first 10 nucleotides of pLN 5'LTR
 (NCBI/Genbank: M28215)
 OTHER INFORMATION: n is a, g, c or t/u
 US-09-830-337-41

Query Match 68.0%; Score 13.6; DB 3; Length 35;
 Best Local Similarity 80.0%; Pred. No. 5.3e+02;
 Matches 16; Conservative 0; Mismatches 4;
 Qy 1 AACATGTAACTTTGCGCA 20
 Db 20 AACTAGTAATTGATCA 1

RESULT 10
 Sequence 14, Application US/09684579
 Patent No. 6670450
 GENERAL INFORMATION:
 APPLICANT: Wadhwa, Renu
 APPLICANT: Kaul, Sunil C.
 APPLICANT: Reddel, Roger R.
 TITLE OF INVENTION: PROTEIN AND GENE INVOLVED IN MYOCYTE DIFFERENTIATION
 FILE REFERENCE: 06501-06501
 CURRENT APPLICATION NUMBER: US/09/684,579
 CURRENT FILING DATE: 2000-11-06
 PRIORITY APPLICATION NUMBER: PCT/JP99/01913
 PRIORITY FILING DATE: 1999-01-09
 PRIORITY APPLICATION NUMBER: JAPAN 10/115975
 PRIORITY FILING DATE: 1998-04-10
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO: 14
 LENGTH: 30
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Primer for PCR
 US-09-684-579-14

Query Match 66.0%; Score 13.2; DB 4; Length 30;
 Best Local Similarity 83.3%; Pred. No. 8.2e+02; 0; Mismatches
 Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 3 ACATGACTTCTTGGCA 20
 Db 28 ACATGAAACATTTAGGCA 11

RESULT 11
 US-03-684-579-16/c
 Sequence 16, Application US/09684579
 ; Patent No. 6570450
 ; GENERAL INFORMATION:
 ; APPLICANT: Madhwa, Renu
 ; APPLICANT: Kaul, Sunil C.
 ; APPLICANT: Reddel, Roger R.
 ; TITLE OF INVENTION: PROTEIN AND GENE INVOLVED IN MYOCYTE
 ; TITLE OF INVENTION: DIFFERENTIATION
 ; FILE REFERENCE: 05501-066001
 ; CURRENT APPLICATION NUMBER: US/09/684,579
 ; CURRENT FILING DATE: 2000-10-05
 ; PRIORITY APPLICATION NUMBER: PCT/JP99/01913
 ; PRIORITY FILING DATE: 1999-04-09
 ; PRIORITY FILING DATE: 1999-04-10
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 16
 ; LENGTH: 31
 ; TYPE: DNA
 ; ORIGIN/SM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: primer for PCR

Qy 09-684-579-16

Query Match 66.0%; Score 13.2; DB 4; Length 31;
 Best Local Similarity 83.3%; Pred. No. 8.3e+02; 0; Mismatches 3; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ACATGACTTCTTGGCA 20
 Db 29 ACATGAAACATTTAGGCA 12

RESULT 12
 US-08-411-389-9
 ; Sequence 9, Application US/08411389
 ; Patent No. 5605799
 ; GENERAL INFORMATION:
 ; APPLICANT: White, Raymond L.
 ; APPLICANT: Cawthon, Richard M.
 ; APPLICANT: Li, Ying
 ; TITLE OF INVENTION: SOMATIC MUTATIONS IN THE
 ; TITLE OF INVENTION: NEUROFIBROMATOSIS TYPE 1 GENE IN HUMAN TUMORS
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 ; STREET: 1201 New York Avenue NW, Suite 1000
 ; CITY: Washington
 ; STATE: DC
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/381,280
 ; CURRENT APPLICATION DATA:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/037,281
 ; FILING DATE: March 26, 1993
 ; APPLICATION NUMBER: 07/929,513
 ; FILING DATE: August 14, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren M. Cheek, Jr.
 ; REGISTRATION NUMBER: 33,367
 ; REFERENCE/DOCKET NUMBER:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-8850
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 27 bases
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; US-08-411-389-9

RESULT 13
 US-08-381-280-20
 ; Sequence 20, Application US/08381280
 ; GENERAL INFORMATION:
 ; APPLICANT: Kazuhiko NISHITANI et al.
 ; TITLE OF INVENTION: ENDO-XYLOGUCAN TRANSFERASE
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wenderoth, Lind & Ponack
 ; STREET: 805 Fifteenth Street, N.W., #700
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: diskette, 5 1/4 inch, 500 kb
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/381,280
 ; CURRENT APPLICATION DATA:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/037,281
 ; FILING DATE: March 26, 1993
 ; APPLICATION NUMBER: 07/929,513
 ; FILING DATE: August 14, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren M. Cheek, Jr.
 ; REGISTRATION NUMBER: 33,367
 ; REFERENCE/DOCKET NUMBER:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-8850
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 27 bases
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid

HYPOTHETICAL:
 ANTI-SENSE:
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HAPLOTYPE:
 TISSUE TYPE:
 CELL TYPE:
 CELL LINE:
 ORGANELLE:
 IMMEDIATE SOURCE:
 LIBRARY:
 CLONE:
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT:
 MAP POSITION:
 UNITS:
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION:
 PUBLICATION INFORMATION:
 AUTHORS:
 TITLE:
 JOURNAL:
 VOLUME:
 ISSUE:
 PAGES:
 DATE:
 DOCUMENT NUMBER:
 FILING DATE:
 PUBLICATION DATE:
 RELEVANT RESIDUES IN SEQ ID NO:
 US-08-381-280-20

RESULT 14

Query Match 63.0%; Score 12.6; DB 1; Length 27;
 Best Local Similarity 78.9%; Pred. No. 1.6e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AACATGTAACCTTGTC 19
 Db 8 AGACATGTAATTAGGCC 26

Query Match 63.0%; Score 12.6; DB 2; Length 27;
 Best Local Similarity 78.9%; Pred. No. 1.6e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AACATGTAACCTTGTC 19
 Db 8 AGACATGTAATTAGGCC 26

RESULT 15

Query Match 63.0%; Score 12.6; DB 2; Length 27;
 Best Local Similarity 78.9%; Pred. No. 1.6e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AACATGTAACCTTGTC 19
 Db 8 AGACATGTAATTAGGCC 26

FILING DATE: January 31, 1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/037,281
 FILING DATE: March 26, 1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/939,513
 FILING DATE: August 14, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren M. Cheek, Jr.
 REGISTRATION NUMBER: 33,367
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-8850
 TELEFAX:
 TELEXX:
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 27 bases
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 HYPOTHETICAL:
 ANTI-SENSE:
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HAPLOTYPE:
 TISSUE TYPE:
 CELL TYPE:
 CELL LINE:
 ORGANELLE:
 IMMEDIATE SOURCE:
 LIBRARY:
 CLONE:
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT:
 MAP POSITION:
 UNITS:
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION:
 PUBLICATION INFORMATION:
 AUTHORS:
 TITLE:
 JOURNAL:
 VOLUME:
 ISSUE:
 PAGES:
 DATE:
 DOCUMENT NUMBER:
 FILING DATE:
 PUBLICATION DATE:
 RELEVANT RESIDUES IN SEQ ID NO:
 US-08-445-533-20

RESULT 15

Query Match 63.0%; Score 12.6; DB 2; Length 27;
 Best Local Similarity 78.9%; Pred. No. 1.6e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AACATGTAACCTTGTC 19
 Db 8 AGACATGTAATTAGGCC 26

Query Match 63.0%; Score 12.6; DB 2; Length 27;
 Best Local Similarity 78.9%; Pred. No. 1.6e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AACATGTAACCTTGTC 19
 Db 8 AGACATGTAATTAGGCC 26

RESULT 15

Query Match 63.0%; Score 12.6; DB 2; Length 27;
 Best Local Similarity 78.9%; Pred. No. 1.6e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AACATGTAACCTTGTC 19
 Db 8 AGACATGTAATTAGGCC 26

FILING DATE: May 22, 1995
 APPLICATION NUMBER: US08/145,533
 FILING DATE: May 22, 1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/381,280

APPLICATION NUMBER: 08/381,280

Patent No. 6120998

GENERAL INFORMATION:

APPLICANT: Katsuhiko NISHITANI et al.

TITLE: ENDO-XYLOGLUCAN TRANSFERASE

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.

STREET: 2033 K Street, N.W., #800

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Disquette, 3.5 inch, 1.44 mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/052,085

FILING DATE: March 31, 1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/445,533

FILING DATE: May 22, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/381,280

FILING DATE: January 31, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/037,281

FILING DATE: March 26, 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/929,513

FILING DATE: August 14, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-721-8200

TELEFAX: 202-721-8250

TELEX:

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

US-09-052-085-20

Query Match 63.0%; Score 12.6; DB 3; Length 27;
 Best Local Similarity 78.9%; Pred. No. 1.6e+03; Mismatches 4;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	1	AAACATGTAATCTTGGTC	19
	8	AGACGTGTTATTTAGGCC	26

Search completed: March 27, 2004, 10:42:14
Job time : 76 sec

PT atherosclerosis.
 XX
 PS Claim 3; Page 85; 139PP; English.
 XX
 CC This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides.
 CC CTGF has been mapped to human chromosome region 6q23.1, and is also known as ctnfract, fibroblast inducible secreted protein, fisp-12, NOV2, PTIGBP-2, CC insulin-like growth factor binding protein-related protein 2, IGFBP-2P2, CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and CC promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial cells.
 CC that inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative disorders (particularly cancer, e.g. breast, prostate or renal cancer), CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As such, the present invention describes these antisense oligos as having cytostatic, dermatological and antiarteriosclerotic activities. This oligonucleotide sequence is a chimeric phosphorothioate antisense oligo with 2', MOE wings and a deoxy gap, which is used to inhibit expression of human CTGF of the invention.
 XX
 Sequence 20 BP; 7 A; 3 C; 3 G; 7 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 20; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.1; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db
 XX
 RESULT 2
 ID ADB25671 standard; DNA; 20 BP.
 XX
 AC ADB25671;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DB Human connective tissue growth factor antisense oligo DNA (seqID 64).
 XX
 KW antisense; human; ss; connective tissue growth factor; CTGF; CC
 KW chromosome 6q23.1; ctnfract; fibroblast inducible secreted protein; CC
 KW fisp-12; NOV2;
 KW insulin-like growth factor binding protein-related protein 2; IGFBP-2P2; CC
 KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
 KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
 KW scleroderma; atherosclerosis; cytostatic; dermatological;
 KW antiarteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT modified_base 1: -20
 FT /*Tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER: phosphorothioate backbone, where 1-5 and
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
 FT 5-methylcytidines"
 XX
 PN WO2003053340-A2.
 XX
 PD 03-JUN-2003.
 XX
 PP 09-DEC-2002; 2002WO-US038618.
 XX
 PR 10-DEC-2001; 2001US-00006191.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Gaarde WA, Watt AT;
 XX
 DR WPI; 2003-559091/52.
 XX
 PT New antisense oligonucleotides for modulating connective tissue growth factor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or atherosclerosis.
 PT
 XX
 PS Claim 3; Page 85; 139PP; English.
 XX
 CC This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides.
 CC CTGF has been mapped to human chromosome region 6q23.1, and is also known as ctnfract, fibroblast inducible secreted protein, fisp-12, NOV2, PTIGBP-2, CC insulin-like growth factor binding protein-related protein 2, IGFBP-2P2, CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and CC promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial cells.
 CC that inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative disorders (particularly cancer, e.g. breast, prostate or renal cancer), CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As such, the present invention describes these antisense oligos as having cytostatic, dermatological and antiarteriosclerotic activities. This oligonucleotide sequence is a chimeric phosphorothioate antisense oligo with 2', MOE wings and a deoxy gap, which is used to inhibit expression of human CTGF of the invention.
 XX
 Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;
 SQ Query Match 95.0%; Score 19; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 9.6; Mismatches 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db
 XX
 RESULT 3
 ACI56439
 ID ACI56439 standard; DNA; 25 BP.
 XX
 AC ACI56439;
 XX
 DT 13-OCT-2003 (first entry)
 XX
 DE Human microarray DNA oligonucleotide SEQ ID NO 56430.
 XX
 EST; ss; probe; expressed sequence tag; microarray; gene expression; CC
 KW genetic variation; biallelic marker; polymorphism; human; cross- species comparison.
 XX
 OS Homo sapiens.
 XX
 PN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (AFFY-) AFFYMETRIX INC.
 XX
 PI Mittmann MP;
 XX
 DR WPI; 2003-567953/53.
 XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot blot hybridization to identify or detect the

PT sequence or specific mutations of any gene.

XX PR 10-DEC-2001; 2001US-00006191.

PS XX

XX PA (ISIS) ISIS PHARM INC.

CC XX

CC Also disclosed is a method of gene expression analysis. The array is used

CC in monitoring gene expression levels by hybridisation to a DNA library,

CC probes are attached to a solid support. The analysis comprises monitoring

CC gene expression levels, identifying biallelic markers or polymorphisms,

CC or family members of a gene, and a cross-species comparison. Each of the

CC nucleic acids further comprises a tag sequence. The array of nucleic acid

CC probes is useful in in situ hybridisation, in Southern, Northern or dot-

CC blot hybridisation to identify or detect the sequence or specific

CC mutations of any gene, in mapping the 5' termini of mRNA molecules by

CC primer extensions or in screening cDNA or genomic libraries or subclones

CC for additional subclones containing segments of DNA that have been

CC isolated and previously sequenced. The sequence presented is one of the

CC nucleic acid probes incorporated in the microarray. Note: The sequence

CC data for this patient can also be obtained in electronic format directly

CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 6 A; 4 C; 4 G; 11 T; 0 U; 0 Other;

XX Query Match 76.0%; Score 15.2; DB 8; Length 25;

XX Best Local Similarity 85.0%; Pred. No. 7.5e+02; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

XX QY 1 AACAGTGTACTTGGTCA 20

XX Db 1 AGACATGTACTTTTCA 20

RESULT 4

XX ADB25654 standard; DNA; 20 BP.

XX AC ADB25654;

XX DT 20-NOV-2003 (first entry)

XX DR Human connective tissue growth factor antisense oligo DNA (seqID 47),
XX KW antisense; human; ss; connective tissue growth factor; CTGF;
XX KW chromosome 5q23.1; ctgfprotein; fibroblast inducible secreted protein;
XX KW FSP-12; NOV2;
XX KW insulin-like growth factor binding protein 2; IGFBP-rP2;
XX KW IGFBP-8; Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
XX KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
XX KW sclerodema; atherosclerosis; cytostatic; dermatological;
XX KW antiarteriosclerotic.
XX OS Homo sapiens.

XX PH Key Location/Qualifiers
XX FT 1. .20
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= phosphorothioate backbone' where 1-5 and
XX FT 16-20 are 2'-methoxyethyl nucleotides. All cytidines are
XX FT 5'-methylcytidines"
XX PN WO2003053340-A2.
XX PD 03-JUL-2003.
XX PI 09-DEC-2002; 2002WO-US038618.

XX PR 10-DEC-2001; 2001US-00006191.

XX XX

XX PA Gaarde WA, Watt AT;

XX DR WPI; 2003-559091/52.

XX XX

XX PT New anti-sense oligonucleotides for modulating connective tissue growth

XX or prostate cancer), pulmonary or renal fibrosis, scleroderma or

XX atherosclerosis.

XX XX

XX PS Claim 3; Page 85; 139pp; English.

XX XX

XX CC This invention relates to novel methods for modulating the expression of

XX connective tissue growth factor (CTGF) by antisense oligonucleotides.

XX CC CTGF has been mapped to human chromosome region 6q23.1, and is also known

XX as ctgfprotein, fibroblast inducible secreted protein, fipf-12, NOV2,

XX insulin-like growth factor binding protein-related protein 2, IGFBP-rP2,

XX IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and

XX promote chemotaxis of fibroblasts, however, it is also upregulated in

XX acute lymphoblastic leukaemia and in tumour or endothelial cell

XX associated with the vasculature. Accordingly, antisense oligonucleotides

XX that inhibit the expression of CTGF in cells or tissues can be used in

XX gene therapy to treat various conditions including hyperproliferative

XX disorders (particularly cancer, e.g. breast, prostate or renal cancer),

XX pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As

XX such, the present invention describes these antisense oligos as having

XX cytostatic, dermatological and antiarteriosclerotic activities. This

XX oligonucleotide sequence is a chimeric phosphorothioate antisense oligo

XX with 2' MOE wings and a deoxy gap, which is used to inhibit expression of

XX human CTGF of the invention.

XX Sequence 20 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

XX Query Match 75.0%; Score 15; DB 8; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 9.3e+02; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 6 TGTAACTTGGTCA 20

XX Db 1 TGTAACCTTGGTCA 15

RESULT 5

XX ID ACI49802/c

XX ID ACTI49802 standard; DNA; 25 BP.

XX AC ACI49802;

XX DT 13-OCT-2003 (first entry)

XX DR Human microarray DNA oligonucleotide SEQ ID NO 49793.

XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX KW genetic variation; biallelic marker; polymorphism; human;
XX KW cross-species comparison.

XX OS Homo sapiens.

XX PN US2003104410-A1.

XX PD 05-JUN-2003.

XX PR 15-MAR-2002; 2002US-00098263.

XX XX

XX PA 16-MAR-2001; 2001US-0276759P.

XX XX

XX PD (AFFY-) AFFYMETRIX INC.

XX XX

XX PI Mittmann MP;

CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in *in situ* hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX

SQ Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 8; Length 25;
 Best Local Similarity 88.9%; Pred. No. 1.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACTGTAACTTGTGCTA 20
 Db 4 ACATGTTACTTTGCTCA 21

RESULT 8
 ACK05946
 ID ACK05946 standard; DNA; 25 BP.
 XX
 AC ACK05946;
 DT 14-OCT-2003 (first entry)
 DE Human microarray DNA oligonucleotide SEQ ID NO 105927.
 XX
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX
 OS Homo sapiens.
 XX
 PN US2003144410-A1.
 XX
 PD 05-JUN-2003.
 XX
 PP 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (AFFY-) AFFYMETRIX INC.
 XX
 PT Mittmann MP;
 XX
 DR WPI; 2003-567953/53.

PT New array of nucleic acid probes, useful for *in situ* hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1; SEQ ID NO 105927; 9pp; English.

CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridization to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis

CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in *in situ* hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX

SQ Sequence 25 BP; 9 A; 4 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 8; Length 25;
 Best Local Similarity 84.2%; Pred. No. 2.4e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACAGTAACTTGTGCTA 20
 Db 6 AAAAGTAACCTGTGCTA 24

RESULT 9
 ADB25670
 ID ADB25670 standard; DNA; 20 BP.
 XX
 AC ADB25670;
 XX
 DT 20-NOV-2003 (first entry)
 DE Human connective tissue growth factor antisense oligo DNA (SeqID 63).
 XX
 KW anti-sense; human; ss; connective tissue growth factor; CTGF;
 KW chromosome 6q23.1; ctgfact; fibroblast inducible secreted protein;
 KW fisp-12; Nov2;
 KW insulin-like growth factor binding protein-related protein 2; IGFBP-rP2;
 KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
 KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
 KW scleroderma; atherosclerosis; cytostatic; dermatological;
 KW antiarteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate backbone; where 1-5 and
 FT 16-20 are 2', methoxyethyl nucleotides. All cytidines are
 FT 5'-methylcytidines"
 XX
 PN WO2003053340-A2.
 XX
 PD 03-JUL-2003.
 XX
 PT 09-DEC-2002; 2002WO-US038618.
 XX
 PR 10-DEC-2001; 2001US-0006191.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Gaarde WA, Watt AT;
 XX
 DR WPI; 2003-559091/52.
 XX
 PT New antisense oligonucleotides for modulating connective tissue growth
 PT factor expression, particularly useful for treating cancers (e.g. breast

PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or atherosclerosis.

XX PS Claim 3, Page 85; 139pp; English.

This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides. CTGF has been mapped to human chromosome region 6q23.1, and is also known as ctfactor, fibroblast inducible secreted protein, fisp-12, NOV2, insulin-like growth factor binding protein-related protein 2, IGFBP-rP2, IGFBP-8, Hs24 and ecogenin. It is known to stimulate DNA synthesis and promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative disorders (particularly cancer, e.g. breast, prostate or renal cancer), pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As such, the present invention describes these antisense oligos as having cytostatic, dermatological and antiarteriosclerotic activities. This oligonucleotide sequence is a chimeric phosphorothioate antisense oligo with 2, MOE wings and a deoxy gap, which is used to inhibit expression of human CTGF of the invention.

XX SQ Sequence 20 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAACTTTGCTCA 20
Db -1 GAACTTTGCTCA 14

RESULT 10
ACI5754/C

ID ACI57654 standard; DNA; 25 BP.

XX AC ACI57654;

XX DT 13-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 57645.

XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.

XX OS Homo sapiens.

XX PN US2003104410-A1.

XX PD 05-JUN-2003.

XX PP 15-MAR-2002; 2002US-00098263.

XX PR 16-MAR-2001; 2001US-0276759P.

XX PA (AFFY-) AFFYMETRIX INC.

XX PI Mittmann MP;

XX DR Mittmann MP;

XX WiFi; 2003-567953/53.

PT New array of nucleic acid probes, useful for in situ hybridization, in PT sequence or specific mutations of any gene.

XX PT Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

XX PS Claim 1; SEQ ID NO 57645; 9pp; English.

CC The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used

CC perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, CC of at least one target sequence. The method of analysis comprises CC nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprise monitoring CC gene expression levels, identifying biallelic markers or polymorphisms, CC or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones CC for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly CC from USPTO at seqdata.uspto.gov/sequence.html

XX SQ Sequence 25 BP; 8 A; 4 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 68.0%; Score 13.6; DB 8; Length 25;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AACATGTAACTTTGCTCA 20
Db 23 AACATGTAACCTTCCTA 4

RESULT 11

ACI1811/C

ID ACI1781 standard; DNA; 25 BP.

XX AC ACI1781;

XX DT 13-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 17802.

XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.

XX OS Homo sapiens.

XX PN US2003104410-A1.

XX PD 05-JUN-2003.

XX PP 15-MAR-2002; 2002US-00098263.

XX PR 16-MAR-2001; 2001US-0276759P.

XX PA (AFFY-) AFFYMETRIX INC.

XX PI Mittmann MP;

XX DR Mittmann MP;

XX WiFi; 2003-567953/53.

PT New array of nucleic acid probes, useful for in situ hybridization, in PT Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

XX PT The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

CC Also disclosed is a method of gene expression analysis. The array is used

CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC nucleic acid probes attached to a solid support. The analysis comprises monitoring
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC nucleic acid probes attached to a solid support. The analysis comprises monitoring
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX Sequence 25 BP; 7 A; 4 C; 7 G; 7 T; 0 U; 0 Other;
 CC Query Match 68.0%; Score 13.6; DB 8; Length 25;
 CC Best Local Similarity 80.0%; Pred. No. 4.7e-03;
 CC Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 CC Qy 1 AACATGTAACCTTGTCA 20
 CC Db 20 AACATGTAACCTTGTCA 1
 RESULT 12
 ACT156438
 ID ACT156438 Standard; DNA; 25 BP.
 XX
 AC ACT156438;
 XX DT 13-OCT-2003 (first entry)
 DE Human microarray DNA oligonucleotide SEQ ID NO 56429.
 XX EST; ss; Probe; expressed sequence tag; microarray; gene expression;
 KW EST; ss; Probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 OS Homo sapiens.
 XX PN US2003104410-A1.
 XX PD 05-JUN-2003.
 XX PF 15-MAR-2002; 2002US-00099263.
 XX PR 16-MAR-2001; 2001US-0276759P.
 XX PA (AFFY-) AFFYMETRIX INC.
 XX PI Mittmann MP;
 XX WPI; 2003-567953/53.
 XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1; SEQ ID NO 56429; 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled

CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC nucleic acid probes attached to a solid support. The analysis comprises monitoring
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX Sequence 25 BP; 7 A; 4 C; 4 G; 10 T; 0 U; 0 Other;
 CC Query Match 68.0%; Score 13.6; DB 8; Length 25;
 CC Best Local Similarity 80.0%; Pred. No. 4.7e-03;
 CC Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 CC Qy 1 AACATGTAACCTTGTCA 20
 CC Db 1 AGACATGTAACCTTGTCA 20
 RESULT 13
 ADD20567/C
 ID ADD20567 Standard; DNA; 25 BP.
 XX
 AC ADD20567;
 XX DT 15-JAN-2004 (first entry)
 DE Oreochromis niloticus microsatellite primer SEQ ID NO:1202.
 XX single nucleotide polymorphism; SNP; fish; *Salmo salar*;
 KW oreochromis niloticus; Atlantic halibut; microsatellite; cod;
 KW polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;
 KW detection; primer; ss.
 XX Synthetic.
 OS Oreochromis niloticus.
 XX PN WO2003060160-A2.
 XX PD 24-JUL-2003.
 XX PF 17-JAN-2003; 2003WO-1B000112.
 XX PR 18-JAN-2002; 2002US-0349950P.
 PR 16-AUG-2002; 2002US-0404200P.
 XX PA (GENO-) GENOMAR ASA.
 XX PI Lie O, Slettan A, Hoyum M, Lingaa F;
 XX DR WPI; 2003-627388/59.
 XX
 PT Novel isolated nucleic acid molecule comprising single nucleotide
 PT polymorphism associated with fish, useful for forming PCR primers which
 PT are used for detecting single nucleotide polymorphisms in fish nucleic
 PT acids.
 XX
 PS Claim 18; SEQ ID NO 1202; 233PP; English.
 XX
 CC The present invention describes an isolated nucleic acid (I) comprising a
 CC single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of
 CC *Salmo salar* SNPs; *Oreochromis niloticus* SNPs or *Atlantic halibut* SNPs;
 CC and (ii) a nucleic acid having nucleotide sequence that hybridises to

CC (i), or its complement under highly stringent hybridization conditions.
 CC Also described: (1) an isolated oligonucleotide (II) comprising at least
 CC 17 contiguous nucleotides of a nucleotide sequence of *S. salar* SNPs, *O.
 CC niloticus* SNPs, *O. niloticus* microsatellites, Atlantic halibut SNPs, cod
 CC polymorphic sites and seabass polymorphic sites, or their complement; (2)
 CC a primer pair (III) suitable for use in PCR, comprising two (III) capable
 CC of amplifying a nucleotide sequence chosen from *S. salar* SNPs and *O.
 CC niloticus* SNPs, *O. niloticus* microsatellites, Atlantic halibut SNPs, cod
 CC polymorphic sites and seabass polymorphic sites; and determining (M1) the
 CC origin of fish sample comprising providing a parentage genotype database
 CC comprising a collection of candidate parent genotypes, where each of the
 CC candidate parent genotype represents a distinct origin, and comparing a
 CC sample genotype to the parentage genotype database, where a match between
 CC the sample genotype and one of the candidate parent genotype identifies
 CC the origin of the sample. (M1) is useful for determining the origin of
 CC a fish sample such as family salmonidae, *S. salar*, *Tilapia*, *O. niloticus*
 CC rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for
 CC detecting nucleic acid molecule comprising SNP in a sample, which
 CC involves contacting the sample containing nucleic acids with one or more
 CC SNPs, and identifying nucleic acid that hybridizes to (II). (II) is
 CC useful for detecting nucleic acid molecule comprising a polymorphic
 CC sequence in a sample, comprising contacting the sample containing nucleic
 CC acids with one or more (II) which is derived from *O. niloticus*
 CC microsatellite, *O. niloticus* SNPs, Atlantic halibut SNPs, cod polymorphic
 CC sites, and seabass polymorphic sites; and identifying a nucleic acid that
 CC hybridizes to (II). (III) is useful for detecting nucleic acid molecule
 CC comprising a microsatellite sequence in sample. The present sequence is
 CC used in the exemplification of the present invention.

SQ Sequence 25 BP; 9 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

Query	1	2	3	4
Qy	AACTGATGACTTGTGTC	20		
Do	23	AGAGHTGACTTGTGTC	4	

RESULT 14

ID	AAQ68537	standard; cDNA; 26 BP.
XX	AAQ68537;	
AC		
DT	25-MAR-2003	(revised)
DT	13-FEB-1995	(first entry)
DB	<i>B.thuringiensis</i> 33KD delta-endotoxin N-terminal probe.	
XX		
KW	Insecticidal protein; delta-endotoxin; crystal; Coleoptera; Lepidoptera;	
KW	<i>Bacillus thuringiensis</i> ; ss.	
OS	Synthetic.	
XX		
PN	WO9413785-A2.	
XX		
PD	23-JUN-1994.	
PP	13-DBC-1993; 93WO-US012144.	
XX		
PR	15-DEC-1992; 92US-0091073.	
XX		
PA	(NOVO) NOVO-NORDISK ENTOTECH INC.	
XX		
PT	Liu, C., Adams, LF., Lubffrow, PA., Thomas, MD;	
PT	WPI; 1994-217865/26.	
PT	New <i>Bacillus thuringiensis</i> strains - which produce new delta-endotoxin	
PT	caps used for the control of lepidopteran and Coleopteran insect pests.	

PS	Example 9; Page 26; 47pp; English.
XX	The N-terminal sequence of a 33kD delta-endotoxin isolated from
CC	<i>B.thuringiensis</i> EMC0075 (NRRL B-21019) or EMC0076 (NRRL B-21020) was
CC	determined (see AAC59764). Based on this sequence a 26mer oligonucleotide
CC	was designed (use as a probe (AAG68537) for cloning the delta-
CC	endotoxin gene. (Updated on 25-MAR-2003 to correct PN field.)
XX	Sequence 26 BP; 13 A; 2 C; 2 G; 9 T; 0 U; 0 Other;
SQ	Query Match 68.0%; Score 13.6; DB 2; Length 26; Best Local Similarity 80.0%; Pred. No. 4.7e+03; Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	1 AACACATGAACTTGTGTC 20
Db	23
XX	RESULT 15
AAT51400	68.0%; Score 13.6; DB 2; Length 26;
ID AAT51400 standard; DNA; 33 BP.	Best Local Similarity 80.0%; Pred. No. 4.7e+03;
XX	Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
AC AAT51400;	23
XX	DT 23-APR-1997 (first entry)
XX	D. <i>immitis</i> VA5-like gene clone nDiVA726 sense primer BvVA sen.
KW	Venom allergen antigen 5-like gene; VA5; helminth; parasite; nDiVA726;
KW	vaccine; heartworm; <i>Dirofilaria immitis</i> ; primer; PCR;
KW	polymerase chain reaction; ss.
XX	Synthetic.
OS	
XX	
PN	
W09637218-A1.	
XX	
PD	
XX	28-NOV-1996.
PF	
XX	23-MAY-1996; 96WO-US0007709.
PR	
XX	23-MAY-1995; 95US0-00450944.
PA	
XX	(HESK-) HESKA CORP.
PI	
XX	Tripp CA, Wisniewski N;
DR	
XX	WPI; 1997-020935/02.
PT	
XX	Nucleic acid encoding helminth venom allergen antigen 5-like protein -
PT	pref. from <i>Dirofilaria immitis</i> or <i>Onchocerca volvulus</i> , useful esp. in
PT	vaccines to prevent helminth infection.
PS	
XX	Example 4; Page 68; 124pp; English.
CC	Sense Primer BvVA sen (AAT51400) contg. a BamHI site, and antisense
CC	primer BvVA ant (AAT51401) contg. a EcoRI site, were used in the PCR
CC	amplification of a 726 nucleotide DNA fragment, designated nDiVA726. This
CC	DNA fragment corresponds to nucleotides 54-779 of the <i>Dirofilaria immitis</i>
CC	nucleic acid molecule nDiVA833 (see also AAT11376), which encodes a venom
CC	allergen antigen 5 (VA5)-like protein (AAW1479). The PCR product was
CC	incorporated into a baculovirus vector to enable prodn. of recombinant
CC	VA5-like protein in <i>Spodoptera frugiperda</i> Sf9 cells
XX	Sequence 33 BP; 9 A; 5 C; 6 G; 13 T; 0 U; 0 Other;
SQ	Query Match 68.0%; Score 13.6; DB 2; Length 33; Best Local Similarity 80.0%; Pred. No. 4.8e+03; Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	1 AACACATGAACTTGTGTC 20
	20

Mon Mar 29 09:29:16 2004

us-10-006-191-48.1150.rng

Page 9

Db 13 AAATATGATACTTTGGTTA 32

Search completed: March 27, 2004, 09:34:17
Job time : 341 secs

ON nucleic - nucleic search, using sw model.

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GenCore version 5.1.6

Run on: March 27, 2004, 09:22:36 ; (without alignments)

Search time 2406 Seconds

248.231 Million cell updates/sec

Title: US-10-006-191-48

Perfect score: 20

Sequence: 1 aaacatgttaactttttggca 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 138346

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: em_esbba:*

2: em_eschum:*

3: em_escort:*

4: em_esmu:*

5: em_esrov:*

6: em_espl:*

7: em_esro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hcc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_escort:*

16: em_esrom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_futn:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rnd:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

§

Result No.	Score	Query Match Length	DB ID	Description
				ALIGMENTS
				RESULT 1
				B2354183/c
				LOCUS
				B2354183
				DEFINITION
				SAALK_123321.19.20.x Arabidopsis thaliana genomic clone
				survey sequence)
				ACCESSION
				B2354183
				VERSION
				GI:24945045
				SOURCE
				Arabidopsis thaliana (thale cress)
				ORGANISM
				Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
				REFERENCE
				1 (bases 1 to 47)
				Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,'Prednis,L.,' Gadrikab,C., Jeske,A., Karnes,M., C.J., Parker,H.,'Prednis,L.,' Shin,P., Zimmerman,J. and Ecker,J.R.
				TITLE
				A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
				JOURNAL
				Unpublished (2001)
				COMMENT
				Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10100 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 6379

Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.

Class: TDNA tagged
 FEATURES source
 Location/Qualifiers

1. .47

/organism="Arabidopsis thaliana"

/mol-type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK 123321-19 20-x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 72.0%; Score 14.4; DB 28; Length 47;
 Best Local Similarity 93.8%; Pred. No. 1 6e+04;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 AAACATGTAACTTTG 16
 Db 40 AACAGTGTAACTTTG 25

RESULT 2

BBH853744 BH853744 40 bp DNA linear GSS 13-JUN-2002
 LOCUS SALK_078203.44.80.x Arabidopsis thaliana TDNA insertion lines
 DEFINITION SALK_078203.44.80.x, genomic survey sequence.

ACCESSION BH853744
 VERSION BH853744.1 GI:21424615

KEYWORDS GSS

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Arabidopsis.

REFERENCE Alonso,J.M., Leisse,T.J., Barrjas,P., Chen,H., Cheuk,R., Prednis,L.,

Gadrinab,C., Jeekle,A., Karnes,M., Kim,C.J., Parker,H., Saedler,H.,

Shinn,P., Zimmerman,J., and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL Unpublished
 CONTACT: Joseph R. ECKER

COMMENT Unpublished

REFERENCE Strizhov,N., Li,Y., Rosso,M. and Weisshaar,B.

JOURNAL Direct Submission

COMMENT Submitted (21-OCT-2002) Weisshaar,B., Max-Planck-Institut fuer

Zuchtforschung, Cari-von-Linne-Weg 10, Koeln, 50929, Germany

REFERENCE This sequence is recovered from the left border of the TDNA. It

indicates an insertion close to or within gene At5g0000. The

sequences are generated at the MPI for Plant Breeding Research in

the context of the GABI-Kat project. GABI-Kat is part of the German

Plant Genomics Program designated 'GABI'. Information on line

availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES source
 Location/Qualifiers

1. .40

/organism="Arabidopsis thaliana"

/mol-type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK 078203.44.80.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 68.0%; Score 13.6; DB 29; Length 42;
 Best Local Similarity 80.0%; Pred. No. 3.8e+04;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AAACATGTAACTTTG 20

Db 2 AAAATATACTTTG 21

RESULT 3

AL194204 AL194204 Arabidopsis thaliana T-DNA flanking sequence GK-262601-014926,
 LOCUS AL194204
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-262601-014926,
 VERSION AL194204.1 GI:24398622

KEYWORDS GSS

SOURCE Arabidopsis thaliana (thale cress)

REFERENCE Arabidopsis thaliana (thale cress)

AUTHORS Strizhov,N., Li,Y., Rosso,M., Viehöver,P., Dekker,K., Saedler,H., and Weisshaar,B.

TITLE A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines

REFERENCE 2
 AUTHORS Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
 TITLE A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics

REFERENCE 3
 AUTHORS Strizhov,N., Li,Y., Rosso,M. and Weisshaar,B.
 TITLE Unpublished

COMMENT Submitted (21-OCT-2002) Weisshaar,B., Max-Planck-Institut fuer Zuchtforschung, Cari-von-Linne-Weg 10, Koeln, 50929, Germany

REFERENCE This sequence is recovered from the left border of the TDNA. It indicates an insertion close to or within gene At5g0000. The

sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics Program designated 'GABI'. Information on line

availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES source
 Location/Qualifiers

1. .42

/organism="Arabidopsis thaliana"

/mol-type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK 078203.44.80.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 68.0%; Score 13.6; DB 29; Length 42;
 Best Local Similarity 80.0%; Pred. No. 3.8e+04;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	1 AACATGTAACTTGGTCA 20	JOURNAL	Unpublished (2000)
Db	2 AACTCGTACCTTGGTCA 21	COMMENT	Contact: Robert B. Weiss University of Utah
RESULT 4		Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA	
BJ04144/C		Tel: 801 585 5606	
LOCUS	BJ04144	Fax: 801 585 7177	
DEFINITION	BJ04144 NTIBB Mochii normalized Xenopus neurula library	Email: dunn@genetics.utah.edu	
ACCESSION	Xenopus laevis cDNA clone XLO12903 3', mRNA sequence.	Insert length: 10000 Std Error: 0.00	
VERSION	BJ04144.1	plate: 002 row: G column: 15	
KEYWORDS	EST.	Seq primer: CGTGTAAACGAGGGCACT	
ORGANISM	Xenopus laevis (African clawed frog)	Class: Plasmid ends	
SOURCE	Xenopus laevis	High quality sequence stop: 40.	
REFERENCE	Bukayto, Metzger, Anzu, Mesobatrachia; Pipidae; Amphi-	Location/Qualifiers	
AUTHORS	Amphibia; Batrachia; Chordata; Craniata; Vertebrata; Buteleostomi; Xenopodidae; Xenopus.	1..40	
TITLE	Expressed genes in X. laevis embryo		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Tadao Shin-i Center For Genetic Resource Information		
1	(bases 1 to 35)		
Kitaeva, A., Terasaki, C., Mochii, M., Ueno, N., Shin-i, T. and			
Konata, Y.			
111 Yata, Misima, Shizuoka 411-8540, Japan			
Tei: 81-559-81-6856			
Fax: 81-559-81-6855			
Email: tshinigenes.nig.ac.jp			
The information of this clone is available through the following URL.			
	http://xenopus.nibb.ac.jp .		
FEATURES	Location/Qualifiers		
Source	1..35		
	/organism="Xenopus laevis"		
	/mol_type="mRNA"		
	/db_xref="Taxon:8355"		
	/clone="XLO12903"		
	/tissue_type="whole embryo"		
	/dev_stage="stage 15"		
	/clone_id="NTIBB Mochii normalized Xenopus neurula library"		
ORIGIN			
RESULT 5			
AZ796505			
LOCUS	AZ796505	40 bp	DNA
DEFINITION	2M0052G16F	linear	GSS 16-FEB-2001
ACCESSION	2M0052G16F		
VERSION	AZ796505		
KEYWORDS	AZ796505.1		
GSS.	GI:12944632		
ORGANISM	Mus musculus (house mouse)		
SOURCE	Mus musculus		
REFERENCE	Bukayto, Metzger, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.		
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meinen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niedenhausen, A., and Wright, D., Weiss, R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
RESULT 6			
BH911929/C			
LOCUS	BH911929	42 bp	DNA
DEFINITION	SALK_073084-32-55-x	linear	GSS 04-SEP-2002
ACCESSION	BH911929		
VERSION	073084-32-55-x		
KEYWORDS	Arabidopsis thaliana genomic clone SALK_073084-32-55-x, Genomic survey sequence.		
GSS.	BH911929.1		
ORGANISM	Arabidopsis thaliana (thale cress)		
SOURCE	Arabidopsis thaliana (thale cress)		
REFERENCE	Bukayto, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; eudicots		
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meinen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niedenhausen, A., and Wright, D., Weiss, R.		
TITLE	A sequence-indexed library of insertion mutations in the		

COMMENT	JOURNAL	FEATURES	SEQUENCE
		Source	
		Location/Qualifiers	
		RIGIN	
		RESULT 12	
		BX659565/c	
		Query Match	61.0%; Score 12.2; DB 29; Length 40;
		DEFINITION	Best Local Similarity 82.4%; Pred. No. 1.7e+05;
		ACCSSION	Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0
		VERSION	
		KEYWORDS	
		SOURCE	
		ORGANISM	
		BX659565	
		BX659565.1	
		GSS	
		Arabidopsis thaliana (thale cress)	
		Arabidopsis thaliana	
		Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid III; Brassicaceae; Arabidopsis; Arabidopsis.	
		1	
		Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.	
		AUTHORS	
		TITLE	A pipeline for automated high-throughput generation of ESTs (flanking sequence tags) from <i>Arabidopsis thaliana</i> T-DNA transformed lines
		JOURNAL	Unpublished
		REFERENCE	2
		AUTHORS	Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
		TITLE	A new <i>Arabidopsis thaliana</i> T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
		JOURNAL	Unpublished
		REFERENCE	3 (bases 1 to 47)
		AUTHORS	Strizhov,N., Rosso,M., Li,Y. and Weisshaar,B.
		TITLE	Direct Submission
		JOURNAL	Submitted (06-OCT-2003) Weisshaar,B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
		COMMENT	This sequence is recovered from the left border of the T-DNA. It is unpublished (2001)
		Contact:	Joseph R. Ecker
		Salk Institute Genomic Analysis laboratory (SIGnAL)	
		The Salk Institute for Biological Studies	
		10010 N. Torrey Pines Road, La Jolla, CA 92037, USA	
		Tel:	858 453 4100 x1752
		Fax:	858 558 6379
		Email:	ecker@salk.edu
		Class:	T-DNA tagged

The sequences are generated at the NBI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics Program designated 'GABI'. Information on line availability can be found at:
<http://www.mpi-zkoeln.mpg.de/GABI-Kat/>.

1. 47
 location/qualifiers
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="Taxon:3702"
 /clone="GK-646510-023086"
 /clone_id="Arabidopsis thaliana T-DNA insertion lines"
 /note="PCR was performed on DNA from *Arabidopsis thaliana* plants (T1) which were transformed with the T-DNA from vector PAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the *A. thaliana* nuclear genome sequence were processed for submission. T-DNA derived sequences were removed".

Query	2 AGCTGACTTCTTGTG	18	Score 61.0%	DB 12.2%	Length 29
Source	32 AACATCTAACCTTGTG	16	Best Local Similarity 82.4%	Model 0.1.8e+03	Mismatches 3
Db			Matches 14;	Conservative 0;	Indels 0;
RESULT 13					
LOCUS	AZ620539				
DEFINITION	1M0421B19	48 bp	DNA	linear	GSS 13-DHG-20000
REFERENCE	clone UDGCLM0421B19	F,	UHGCM	library	Mus musculus genomic
ACCESSION	AZ620539				
VERSION	AZ620539.1				
KEYWORDS	GSS.				
SOURCE	Mus musculus	(house mouse)			
ORGANISM	Mus musculus				
	Bukay-Yoata, Metzcoa, Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 48)				
	Dunn,D., Royagi,A., Barber,M., Beacon,T., Duval,B., Hainl,C.,				
	Islam,H., Longacre,S., Mahmoud,M., Meinen,E., Pedersen,T.,				
	Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von				
	Niedzchaein,A. and Wright,D., Weiss,R.				
TITLE	Mouse whole genome scaffolding with Paired end reads from 10kb				
PLASMID	Plasmid				
COMMENT	Unpublished (2000)				
	Contact: Robert B. Weiss				
	University of Utah Genome Center				
	University of Utah				
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT				
	84112, USA				
	Tel: 801 585 5506				
	Fax: 801 585 7777				
	Email: ddunn@genetics.utah.edu				
FEATURES	Insert Length: 10000	Std Error: 0.00			
	Insert: 0421	row: B	column: 19		
	Seq primer: CGTGTAAACGAGGCCAGT				
	Class: plasmid ends				
	High quality sequence stop: 48.				
	location/Qualifiers				
	1 .48				
	/organism="Mus musculus"				
	/mol_type="genomic DNA"				
	/strain="C57BL/6J"				
	/ab_xref="taxon:10090"				

/clone="UJGCIM0421B19"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, λ -resistant, F-

/clone_lib="Mouse 10kb Plasmid UJGCIM library"

/note="Vector: PW42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.Jax.org/resources/documents/dnare/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PW42 (GI:473214|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 61.0%; Score 12.2; DB 28; Length 49;

Best Local Similarity 82.4%; Pred. No. 1.8e+05; Mismatches

14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 25 AACATGTAACATTG 41

/clone lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tDNA_protocols.html"

ORIGIN

Query Match 61.0%; Score 12.2; DB 28; Length 49;

Best Local Similarity 82.4%; Pred. No. 1.8e+05; Mismatches

14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 25 AACATGTAACATTG 41

RESULT 15

Query Match 61.0%; Score 12.2; DB 28; Length 49;

Best Local Similarity 82.4%; Pred. No. 1.8e+05; Mismatches

14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 25 AACATGTAACATTG 41

RESULT 14

Query Match 61.0%; Score 12.2; DB 28; Length 49;

Best Local Similarity 82.4%; Pred. No. 1.8e+05; Mismatches

14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 25 AACATGTAACATTG 41

ORIGIN

Query Match 61.0%; Score 12.2; DB 28; Length 49;

Best Local Similarity 82.4%; Pred. No. 1.8e+05; Mismatches

14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 25 AACATGTAACATTG 41

ORIGIN

Query Match 61.0%; Score 12.2; DB 29; Length 49;

Best Local Similarity 82.4%; Pred. No. 1.8e+05; Mismatches

14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 25 AACATGTAACATTG 41

ORIGIN

Query Match 61.0%; Score 12.2; DB 29; Length 49;

Best Local Similarity 82.4%; Pred. No. 1.8e+05; Mismatches

14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 25 AACATGTAACATTG 41

ORIGIN

Query Match 61.0%; Score 12.2; DB 29; Length 49;

Best Local Similarity 82.4%; Pred. No. 1.8e+05; Mismatches

14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 25 AACATGTAACATTG 41

ORIGIN

Query Match 61.0%; Score 12.2; DB 29; Length 49;

Best Local Similarity 82.4%; Pred. No. 1.8e+05; Mismatches

14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 25 AACATGTAACATTG 41

ORIGIN

Query Match 61.0%; Score 12.2; DB 29; Length 49;

Best Local Similarity 82.4%; Pred. No. 1.8e+05; Mismatches

14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 25 AACATGTAACATTG 41

ORIGIN

Query Match 61.0%; Score 12.2; DB 29; Length 49;

Best Local Similarity 82.4%; Pred. No. 1.8e+05; Mismatches

14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 25 AACATGTAACATTG 41

ORIGIN

Query Match 61.0%; Score 12.2; DB 29; Length 49;

Best Local Similarity 82.4%; Pred. No. 1.8e+05; Mismatches

14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 25 AACATGTAACATTG 41

ORIGIN

Query Match 61.0%; Score 12.2; DB 29; Length 49;

Best Local Similarity 82.4%; Pred. No. 1.8e+05; Mismatches

14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 25 AACATGTAACATTG 41

ORIGIN

Query Match 61.0%; Score 12.2; DB 29; Length 49;

Best Local Similarity 82.4%; Pred. No. 1.8e+05; Mismatches

14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 25 AACATGTAACATTG 41

COMMENT

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Fax: 858 558 6379

Email: ecker@salk.edu

A sequence indexed library of insertion mutations in the Arabidopsis genome

Unpublished

(2001)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,

Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H.,

Shim, P., Zimmerman, J., and Ecker, J.R.,

A sequence indexed library of insertion mutations in the

Arabidopsis genome

Unpublished

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,

Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H.,

Shim, P., Zimmerman, J., and Ecker, J.R.,

A sequence indexed library of insertion mutations in the

Arabidopsis genome

Unpublished

FEATURES

source

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

JOURNAL

FEATURES

SOURCE

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

FEATURES

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JOURNAL

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FEATURES

SOURCE

KEYWORDS

ORG

Mon Mar 29 09:29:17 2004

us-10-006-191-48.1150.rst

Page 8

Search completed: March 27, 2004, 10:40:47
Job time : 2410 secs

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 27, 2004, 09:28:31 ; Search time 266 Seconds

Without alignments) 279.926 Million cell updates/sec

Title: US-10-006-191-48

Perfect score: 20

Sequence: 1 aaacatgttaactttttggtca 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext: 1.0

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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3: /cgtn2_6/prodata/2/pubpna/us06_PUBCOMB.seq:*

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5: /cgtn2_6/prodata/2/pubpna/us07_PUBCOMB.seq:*

6: /cgtn2_6/prodata/2/pubpna/PCTUS_PUBCOMB.seq:*

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8: /cgtn2_6/prodata/2/pubpna/us08_PUBCOMB.seq:*

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11: /cgtn2_6/prodata/2/pubpna/us09c_PUBCOMB.seq:*

12: /cgtn2_6/prodata/2/pubpna/us09c_PUBCOMB.seq:*

13: /cgtn2_6/prodata/2/pubpna/us09c_PUBCOMB.seq:*

14: /cgtn2_6/prodata/2/pubpna/us10c_PUBCOMB.seq:*

15: /cgtn2_6/prodata/2/pubpna/us10c_PUBCOMB.seq:*

16: /cgtn2_6/prodata/2/pubpna/us10c_PUBCOMB.seq:*

17: /cgtn2_6/prodata/2/pubpna/us60_NEW_PUB.seq:*

18: /cgtn2_6/prodata/2/pubpna/us60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
US-10-006-191-48
; Sequence 48, Application US/10006191
; Publication No US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006.191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 48
; LENGTH: 20
; SEQ ID NO 48
; TYPE: DNA
; FEATURE: OTHER INFORMATION: Artificial Sequence
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Antisense Oligonucleotide

US-10-006-191-48

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	20	100.0	20	14 US-10-006-191-48
2	19	95.0	20	14 US-10-006-191-64
3	15.2	76.0	25	14 US-10-098-263B-56430
4	15	75.0	20	14 US-10-006-191-47
5	15	75.0	25	14 US-10-098-263B-49793
6	14	74.0	25	10 US-09-770-07-87
7	14.8	74.0	25	14 US-10-098-263B-15896
8	14.8	74.0	25	14 US-10-349-143-2459
9	14.2	71.0	25	14 US-10-098-263B-05927
10	14	70.0	20	14 US-10-006-191-63
11	13.6	68.0	25	14 US-10-098-263B-7802
12	13.6	68.0	25	14 US-10-098-263B-59429
13	13.6	68.0	25	14 US-10-098-263B-57645
14	13.6	68.0	35	10 US-09-349-143-2459
15	13.6	68.0	35	10 US-09-201-396-10

%; Sequence 64, Application US/10006191
%; Publication No US20030144223A1
%; GENERAL INFORMATION:
%; APPLICANT: William Gaarde
%; APPLICANT: Andrew T. Watt
%; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
%; FILE REFERENCE: RTS-0274
%; CURRENT APPLICATION NUMBER: US/10/006.191
%; CURRENT FILING DATE: 2001-12-10
%; NUMBER OF SEQ ID NOS: 153
%; SEQ ID NO 48
%; LENGTH: 20

Query Match 100.0%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4%; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Sequence 48, Appl

Qy 1 AACATGTAACTTGTGCA 20
Db 1 AAACATGTAACTTGTGCA 20

RESULT 2

Sequence 6, Appl
Sequence 10, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 30, Appl
Sequence 31, Appl
Sequence 32, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 35, Appl
Sequence 36, Appl
Sequence 37, Appl
Sequence 38, Appl
Sequence 39, Appl
Sequence 40, Appl
Sequence 41, Appl
Sequence 42, Appl
Sequence 43, Appl
Sequence 44, Appl
Sequence 45, Appl

Sequence 16, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 30, Appl
Sequence 31, Appl
Sequence 32, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 35, Appl
Sequence 36, Appl
Sequence 37, Appl
Sequence 38, Appl
Sequence 39, Appl
Sequence 40, Appl
Sequence 41, Appl
Sequence 42, Appl
Sequence 43, Appl
Sequence 44, Appl
Sequence 45, Appl

Sequence 147, Appl
Sequence 193, Appl
Sequence 703, Appl
Sequence 879, Appl
Sequence 1805, Appl
Sequence 1928, Appl
Sequence 130406, Appl
Sequence 29, Appl
Sequence 56, Appl
Sequence 412, Appl
Sequence 2187, Appl
Sequence 31651, Appl
Sequence 94449, Appl

CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-10-006-191-64

Query Match 95.0%; Score 19; DB 14; Length 20;
; Best Local Similarity 100.0%; Pred. No. 19; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Qy 1 AACATGTAACTTGGTC 19
; Db 2 AACATGTAACTTGGTC 20

RESULT 3
; US-10-098-263B-56430
; Sequence 56430, Application US/10098263B
; Publication No. US2003010410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 56430
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-098-263B-56430

Query Match 76.0%; Score 15.2; DB 14; Length 25;
; Best Local Similarity 85.0%; Pred. No. 1.3e+03; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
; Qy 1 AACATGTAACTTGGTC 20
; Db 1 AGACATGTAACTTGGTC 20

RESULT 4
; US-10-006-191-47
; Sequence 47, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-10-006-191-47

Query Match 75.0%; Score 15; DB 14; Length 20;
; Best Local Similarity 100.0%; Pred. No. 1.5e+03; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Qy 1 AACATGTAACTTGGTC 19
; Db 2 AACATGTAACTTGGTC 20

RESULT 5
; US-10-098-263B-49793/C
; Sequence 49793, Application US/10098263B
; Publication No. US2003010410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118_1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 49793
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-098-263B-49793

Query Match 75.0%; Score 15; DB 14; Length 25;
; Best Local Similarity 100.0%; Pred. No. 1.6e+03; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Qy 1 AACATGTAACTTGGTC 17
; Db 15 ACATGTAACTTGG 1

RESULT 6
; US-09-770-107-87/C
; Sequence 87, Application US/09770107
; Publication No. US20030054345A1
; GENERAL INFORMATION:
; APPLICANT: Millenium Pharmaceuticals, Inc.
; APPLICANT: Meyer, Joanne
; APPLICANT: Parker, Alexander
; APPLICANT: Barrington-Martin, Rory
; APPLICANT: Barnes, Glein
; APPLICANT: Barrington-Martin, Rory
; TITLE OF INVENTION: Compositions and methods for the diagnosis and treatment of
; FILE REFERENCE: 3322/0H401
; CURRENT APPLICATION NUMBER: US/09/770,107
; CURRENT FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 87
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-09-770-107-87

Query Match 74.0%; Score 14.8; DB 10; Length 25;
; Best Local Similarity 88.9%; Pred. No. 2e+03; Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
; Qy 1 AACATGTAACTTGGTC 18
; Db 21 AACATGTAACGGTGGT 4

RESULT 7
; US-10-098-263B-15896
; Sequence 15896, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1
 CURRENT APPLICATION NUMBER: US/10/098,263B
 CURRENT FILING DATE: 2003-01-08
 PRIOR APPLICATION NUMBER: 60/276,759
 PRIOR FILING DATE: 2001-03-15
 NUMBER OF SEQ ID NOS: 131066
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO: 18996
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapien

US-10-098-263B-15896
 Query Match: 74.0%; Score 14.8; DB 14; Length 25;
 Best Local Similarity 88.9%; Pred. No. 2e+03; 2; Mismatches 0;
 Matches 16; Conservative 0; Indels 0; Gaps 0;
 Qy 3 ACATGTAACTTTGCGCA 20
 Db 4 ACATGTAACTTTGCGCA 21

RESULT 8
 US-10-349-143-469/c
 Sequence 2469, Application US/10349143
 Publication No. US20040005584A1
 GENERAL INFORMATION
 APPLICANT: Cohen, Daniel
 APPLICANT: Blumenfeld, Marta
 APPLICANT: Chumakov, Ilya
 TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
 FILE REFERENCE: GENSET-020CP1
 CURRENT APPLICATION NUMBER: US/10/349,143
 CURRENT FILING DATE: 2003-01-21
 PRIOR APPLICATION NUMBER: US/09/422,978
 PRIOR FILING DATE: 1999-10-20
 PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-04-21
 PRIOR APPLICATION NUMBER: EARLIER FILING DATE: US 60/109,732
 PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
 PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
 NUMBER OF SEQ ID NOS: 11796
 SEQ ID NO: 2469
 LENGTH: 47
 TYPE: DNA
 ORGANISM: Homo Sapiens

FEATURE:
 NAME/KEY: allele
 LOCATION: 24
 OTHER INFORMATION: 99-11179-239 : polymorphic base C or T

US-10-349-143-2469
 Query Match: 74.0%; Score 14.8; DB 15; Length 47;
 Best Local Similarity 80.0%; Pred. No. 2.2e+03; 3; Mismatches 3;
 Matches 16; Conservative 1; Indels 0; Gaps 0;
 Qy 1 AACATGTAACTTTGCGCA 20
 Db 33 AACATGTAACTTTGCGCA 14

RESULT 10
 US-10-006-191-63
 Sequence 63, Application US/10006191
 Publication No. US20030144223A1
 GENERAL INFORMATION
 APPLICANT: William Gaarde
 TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
 FILE REFERENCE: RIS-024
 CURRENT APPLICATION NUMBER: US/10/006,191
 CURRENT FILING DATE: 2001-12-10
 NUMBER OF SEQ ID NOS: 153
 SEQ ID NO: 63
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Antisense Oligonucleotide

US-10-006-191-63
 Query Match: 70.0%; Score 14; DB 14; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.5e+03; 0; Mismatches 0;
 Matches 14; Conservative 0; Indels 0; Gaps 0;
 Qy 7 GTAACTTTGGCGCA 20
 Db 1 GTAACTTTGGCGCA 14

RESULT 11
 US-10-098-263B-17802/c
 Sequence 17802, Application US/10098263B
 Publication No. US20030104410A1
 GENERAL INFORMATION
 APPLICANT: Mittman, Michael
 TITLE OF INVENTION: Human Microarray
 FILE REFERENCE: 3118.1
 CURRENT APPLICATION NUMBER: US/10/098,263B
 CURRENT FILING DATE: 2003-01-08
 PRIOR APPLICATION NUMBER: 60/276,759
 PRIOR FILING DATE: 2001-03-16
 NUMBER OF SEQ ID NOS: 131066
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO: 17802
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo Sapien

US-10-098-263B-17802
 Query Match: 68.0%; Score 13.6; DB 14; Length 25;
 Best Local Similarity 80.0%; Pred. No. 7.3e+03; 4; Mismatches 4;
 Matches 16; Conservative 0; Indels 0; Gaps 0;
 Qy 1 AACATGTAACTTTGCGCA 20

Db 20 AACATCTACTTCGTTGA 1

RESULT 12

US-10-098-263B-56429

; Sequence 56429, Application US/10098263B

; Publication No. US20030104410A1

; GENERAL INFORMATION:

; APPLICANT: Mittman, Michael

; TITLE OF INVENTION: Human Microarray

; FILE REFERENCE: 3118_1

; CURRENT APPLICATION NUMBER: US/10/098, 263B

; CURRENT FILING DATE: 2003-01-08

; PRIOR APPLICATION NUMBER: 60/276, 759

; PRIOR FILING DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 111066

; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1

; SEQ ID NO 56429

; LENGTH: 25

; ORGANISM: Homo sapien

US-10-098-263B-56429

Query Match

Best Local Similarity 68.0%; Score 13.6; DB 14; Length 25;

Matches 16; Conservative 0; Pred. No. 7.3e+03; 4; Indels 0; Gaps 0;

Qy 1 AACATCTACTTCGTTGA 20

Db 1 AGACATGTAACATTTCGA 20

RESULT 13

US-10-098-263B-57645/C

; Sequence 57645, Application US/10098263B

; Publication No. US20030104410A1

; GENERAL INFORMATION:

; APPLICANT: Mittman, Michael

; TITLE OF INVENTION: Human Microarray

; FILE REFERENCE: 3118_1

; CURRENT APPLICATION NUMBER: US/10/098, 263B

; CURRENT FILING DATE: 2003-01-08

; PRIOR APPLICATION NUMBER: 60/276, 759

; PRIOR FILING DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 111065

; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1

; SEQ ID NO 57645

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapien

US-10-098-263B-57645

Query Match

Best Local Similarity 68.0%; Score 13.6; DB 14; Length 25;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AACATGTAACATTTCGTTGA 20

Db 23 AACATGTAACATTTCGA 4

RESULT 14

US-09-309-195-15/C

; Sequence 15, Application US/09309195

; Publication No. US2003000380A1

; GENERAL INFORMATION:

; APPLICANT: FOWKES, Dana M.

; APPLICANT: BROACH, Jim

; APPLICANT: MANFREDI, John

; APPLICANT: KURIN, Christine

; APPLICANT: MURPHY, Andrew J.

; APPLICANT: PAUL, Jeremy

; APPLICANT: TRUEHART, Joshua

Query Match

Best Local Similarity 68.0%; Score 13.6; DB 14; Length 25;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AACATGTAACATTTCGTTGA 20

Db 20 AACATGTAACATTTCGA 1

RESULT 15

US-09-201-396-10/C

; Sequence 10, Application US/09301396A

; Publication No. US2003000902A1

; GENERAL INFORMATION:

; APPLICANT: Klein, Christine A.

; APPLICANT: Murphy, Andrew J.

; APPLICANT: Paul, Jeremy

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RECEPTOR EFFECTORS

; FILE REFERENCE: CPI-012CP9

; CURRENT APPLICATION NUMBER: US/09/201,396A

; CURRENT FILING DATE: 1998-11-30

; EARLIER APPLICATION NUMBER: 08/582,333

; EARLIER FILING DATE: 1996-01-17

; EARLIER APPLICATION NUMBER: 08/322,137

; EARLIER FILING DATE: 1994-10-13

; EARLIER APPLICATION NUMBER: 08/309, 313

; EARLIER FILING DATE: 1994-09-20

; EARLIER APPLICATION NUMBER: 08/190,328
; EARLIER FILING DATE: 1994-01-31
; EARLIER APPLICATION NUMBER: 08/041,431
; EARLIER FILING DATE: 1993-03-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 10
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: Construct
US-09-201-396-10

Query Match 68.0%; Score 13.6; DB 10; Length 35;
Best Local Similarity 80.0%; Pred. No. 7, 7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 AACATGACATTTGGCA 20
Db 20 AAACTGAAATTGATCA 1

Search completed: March 27, 2004, 0:46:54
Job time : 267 secs